RAW SEQUENCE LISTING
PATENT APPLICATION US/08/236,208

DATE: 01/05/96
TIME: 15:16:30

INPUT SET: S8120.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

SEQUENCE LISTING

(1) General Information:

(i)APPLICANT: Evans, Mark J.
Matis, Louis A.
Mueller, Eileen Elliott
Nye, Steven H.
Rollins, Scott
Rother, Russell P.
Springhorn, Jeremy P.
Squinto, Stephen P.
Thomas, Thomas C.
Wilkins, James A.

(ii)TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:
(A)ADDRESSEE: Seth A. Fidel
(B)STREET: 25 Science Park (Alexion)
(C)CITY: New Haven
(D)STATE: Connecticut
(E)COUNTRY: USA
(F)ZIP: 06511

(v)COMPUTER READABLE FORM:
(A)MEDIUM TYPE: 3.5 inch, 1.4Mb storage
(B)COMPUTER: Macintosh Cetris 610
(C)OPERATING SYSTEM: System 7
(D)SOFTWARE: WordPerfect 3.0
(vi)CURRENT APPLICATION DATA:
--> **(A)APPLICATION NUMBER:** ~~08/487,283~~
(B)FILING DATE: June 7, 1995
(vii)PRIOR APPLICATION DATA:
(A)APPLICATION NUMBER: US 08/236,208
(B)FILING DATE: 02-MAY-1994

(viii)ATTORNEY/AGENT INFORMATION:
(A)NAME: Seth A. Fidel.
(B)REGISTRATION NUMBER: 38,449
(C)REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
(ix)TELECOMMUNICATION INFORMATION:

(A)TELEPHONE: (203)776-1790
(B)TELEFAX: (203)772-3655

ERRORED SEQUENCES FOLLOW:

place this main heading over subheading (A) Description:

(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(i) Molecule Type:

--> **(A) DESCRIPTION: KSSKC peptide**
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Ile Asp His Gln Gly Thr Lys Ser Ser
5 10

Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
15 20

---

(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:

include in this count the negative numbers (1676)

--> **(A) LENGTH: 1658 Amino Acids**
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(i) Molecule Type:

--> **(A)DESCRIPTION: Pro-C5 Polytpeptide**
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: No
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Haviland, D.L.
Haviland, J.C.
Fleischer, D.T.
Hunt, A.
Wetsel, R.A.

(B) TITLE: Complete cDNA Sequence of Human
Complement Pro-C5
(C) JOURNAL: Journal of Immunology
(D) VOLUME: 146

(F) PAGES: 362-368
(G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
                 Met Gly Leu Leu Gly Ile Leu Cys Phe Leu
                                -15                 -10

Ile Phe Leu Gly Lys Thr Trp Gly Gln Glu Gln Thr Tyr Val
             -5                -1                   5

Ile Ser Ala Pro Lys Ile Phe Arg Val Gly Ala Ser Glu Asn
             10                  15                  20

Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe Asp Ala
                  25                  30

Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr
 35                  40                  45

Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln
      50                  55                  60

Asn Ser Ala Ile Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly
          65                  70                  75

Gly Gln Asn Pro Val Ser Tyr Val Tyr Leu Glu Val Val Ser
             80                  85                  90

Lys His Phe Ser Lys Ser Lys Arg Met Pro Ile Thr Tyr Asp
                  95                 100

Asn Gly Phe Leu Phe Ile His Thr Asp Lys Pro Val Tyr Thr
105                 110                 115

Pro Asp Gln Ser Val Lys Val Arg Val Tyr Ser Leu Asn Asp
     120                 125                 130

Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr Phe Ile
          135                 140                 145

Asp Pro Glu Gly Ser Glu Val Asp Met Val Glu Glu Ile Asp
             150                 155                 160

His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser
                  165                 170

Asn Pro Arg Tyr Gly Met Trp Thr Ile Lys Ala Lys Tyr Lys
175                 180                 185

Glu Asp Phe Ser Thr Thr Gly Thr Ala Tyr Phe Glu Val Lys
     190                 195                 200
```

```
145
146   Glu Tyr Val Leu Pro His Phe Ser Val Ser Ile Glu Pro Glu
147            205                 210                 215
148
149   Tyr Asn Phe Ile Gly Tyr Lys Asn Phe Lys Asn Phe Glu Ile
150                220                 225                 230
151
152   Thr Ile Lys Ala Arg Tyr Phe Tyr Asn Lys Val Val Thr Glu
153                    235                 240
154
155   Ala Asp Val Tyr Ile Thr Phe Gly Ile Arg Glu Asp Leu Lys
156   245                     250                 255
157
158   Asp Asp Gln Lys Glu Met Met Gln Thr Ala Met Gln Asn Thr
159       260                     265                 270
160
161   Met Leu Ile Asn Gly Ile Ala Gln Val Thr Phe Asp Ser Glu
162            275                 280                 285
163
164   Thr Ala Val Lys Glu Leu Ser Tyr Tyr Ser Leu Glu Asp Leu
165                290                 295                 300
166
167   Asn Asn Lys Tyr Leu Tyr Ile Ala Val Thr Val Ile Glu Ser
168                    305                 310
169
170   Thr Gly Gly Phe Ser Glu Glu Ala Glu Ile Pro Gly Ile Lys
171   315                     320                 325
172
173   Tyr Val Leu Ser Pro Tyr Lys Leu Asn Leu Val Ala Thr Pro
174       330                     335                 340
175
176   Leu Phe Leu Lys Pro Gly Ile Pro Tyr Pro Ile Lys Val Gln
177            345                 350                 355
178
179   Val Lys Asp Ser Leu Asp Gln Leu Val Gly Gly Val Pro Val
180                360                 365                 370
181
182   Ile Leu Asn Ala Gln Thr Ile Asp Val Asn Gln Glu Thr Ser
183                    375                 380
184
185   Asp Leu Asp Pro Ser Lys Ser Val Thr Arg Val Asp Asp Gly
186   385                     390                 395
187
188   Val Ala Ser Phe Val Leu Asn Leu Pro Ser Gly Val Thr Val
189       400                     405                 410
190
191   Leu Glu Phe Asn Val Lys Thr Asp Ala Pro Asp Leu Pro Glu
192            415                 420                 425
193
194   Glu Asn Gln Ala Arg Glu Gly Tyr Arg Ala Ile Ala Tyr Ser
195                430                 435                 440
196
197   Ser Leu Ser Gln Ser Tyr Leu Tyr Ile Asp Trp Thr Asp Asn
```

```
                  445                 450
His Lys Ala Leu Leu Val Gly Glu His Leu Asn Ile Ile Val
455                 460                 465

Thr Pro Lys Ser Pro Tyr Ile Asp Lys Ile Thr His Tyr Asn
    470                 475                 480

Tyr Leu Ile Leu Ser Lys Gly Lys Ile Ile His Phe Gly Thr
        485                 490                 495

Arg Glu Lys Phe Ser Asp Ala Ser Tyr Gln Ser Ile Asn Ile
            500                 505                 510

Pro Val Thr Gln Asn Met Val Pro Ser Ser Arg Leu Leu Val
                515                 520

Tyr Tyr Ile Val Thr Gly Glu Gln Thr Ala Glu Leu Val Ser
525                 530                 535

Asp Ser Val Trp Leu Asn Ile Glu Glu Lys Cys Gly Asn Gln
    540                 545                 550

Leu Gln Val His Leu Ser Pro Asp Ala Asp Ala Tyr Ser Pro
        555                 560                 565

Gly Gln Thr Val Ser Leu Asn Met Ala Thr Gly Met Asp Ser
            570                 575                 580

Trp Val Ala Leu Ala Ala Val Asp Ser Ala Val Tyr Gly Val
                585                 590

Gln Arg Gly Ala Lys Lys Pro Leu Glu Arg Val Phe Gln Phe
595                 600                 605

Leu Glu Lys Ser Asp Leu Gly Cys Gly Ala Gly Gly Gly Leu
    610                 615                 620

Asn Asn Ala Asn Val Phe His Leu Ala Gly Leu Thr Phe Leu
        625                 630                 635

Thr Asn Ala Asn Ala Asp Asp Ser Gln Glu Asn Asp Glu Pro
            640                 645                 650

Cys Lys Glu Ile Leu Arg Pro Arg Arg Thr Leu Gln Lys Lys
                655                 660

Ile Glu Glu Ile Ala Ala Lys Tyr Lys His Ser Val Val Lys
665                 670                 675

Lys Cys Cys Tyr Asp Gly Ala Cys Val Asn Asn Asp Glu Thr
    680                 685                 690
```

```
251  Cys Glu Gln Arg Ala Ala Arg Ile Ser Leu Gly Pro Arg Cys
252           695                 700                 705
253
254  Ile Lys Ala Phe Thr Glu Cys Cys Val Val Ala Ser Gln Leu
255               710                 715                 720
256
257  Arg Ala Asn Ile Ser His Lys Asp Met Gln Leu Gly Arg Leu
258                   725                 730
259
260  His Met Lys Thr Leu Leu Pro Val Ser Lys Pro Glu Ile Arg
261  735                   740                 745
262
263  Ser Tyr Phe Pro Glu Ser Trp Leu Trp Glu Val His Leu Val
264      750                 755                 760
265
266  Pro Arg Arg Lys Gln Leu Gln Phe Ala Leu Pro Asp Ser Leu
267           765                 770                 775
268
269  Thr Thr Trp Glu Ile Gln Gly Ile Gly Ile Ser Asn Thr Gly
270               780                 785                 790
271
272  Ile Cys Val Ala Asp Thr Val Lys Ala Lys Val Phe Lys Asp
273                   795                 800
274
275  Val Phe Leu Glu Met Asn Ile Pro Tyr Ser Val Val Arg Gly
276  805                   810                 815
277
278  Glu Gln Ile Gln Leu Lys Gly Thr Val Tyr Asn Tyr Arg Thr
279      820                 825                 830
280
281  Ser Gly Met Gln Phe Cys Val Lys Met Ser Ala Val Glu Gly
282           835                 840                 845
283
284  Ile Cys Thr Ser Glu Ser Pro Val Ile Asp His Gln Gly Thr
285               850                 855                 860
286
287
288  Lys Ser Ser Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
289                   865                 870
290
291  Ser His Leu Val Thr Phe Thr Val Leu Pro Leu Glu Ile Gly
292  875                   880                 885
293
294  Leu His Asn Ile Asn Phe Ser Leu Glu Thr Trp Phe Gly Lys
295      890                 895                 900
296
297  Glu Ile Leu Val Lys Thr Leu Arg Val Val Pro Glu Gly Val
298           905                 910                 915
299
300  Lys Arg Glu Ser Tyr Ser Gly Val Thr Leu Asp Pro Arg Gly
301               920                 925                 930
302
303  Ile Tyr Gly Thr Ile Ser Arg Arg Lys Glu Phe Pro Tyr Arg
```

```
                  935                 940
Ile Pro Leu Asp Leu Val Pro Lys Thr Glu Ile Lys Arg Ile
945                 950                 955
Leu Ser Val Lys Gly Leu Leu Val Gly Glu Ile Leu Ser Ala
    960                 965                 970
Val Leu Ser Gln Glu Gly Ile Asn Ile Leu Thr His Leu Pro
         975                 980                 985
Lys Gly Ser Ala Glu Ala Glu Leu Met Ser Val Val Pro Val
              990                 995                1000
Phe Tyr Val Phe His Tyr Leu Glu Thr Gly Asn His Trp Asn
                 1005                1010
Ile Phe His Ser Asp Pro Leu Ile Glu Lys Gln Lys Leu Lys
1015                1020                1025
Lys Lys Leu Lys Glu Gly Met Leu Ser Ile Met Ser Tyr Arg
    1030                1035                1040
Asn Ala Asp Tyr Ser Tyr Ser Val Trp Lys Gly Gly Ser Ala
         1045                1050                1055
Ser Thr Trp Leu Thr Ala Phe Ala Leu Arg Val Leu Gly Gln
              1060                1065                1070
Val Asn Lys Tyr Val Glu Gln Asn Gln Asn Ser Ile Cys Asn
                 1075                1080
Ser Leu Leu Trp Leu Val Glu Asn Tyr Gln Leu Asp Asn Gly
1085                1090                1095
Ser Phe Lys Glu Asn Ser Gln Tyr Gln Pro Ile Lys Leu Gln
    1100                1105                1110
Gly Thr Leu Pro Val Glu Ala Arg Glu Asn Ser Leu Tyr Leu
         1115                1120                1125
Thr Ala Phe Thr Val Ile Gly Ile Arg Lys Ala Phe Asp Ile
              1130                1135                1140
Cys Pro Leu Val Lys Ile Asp Thr Ala Leu Ile Lys Ala Asp
                 1145                1150
Asn Phe Leu Leu Glu Asn Thr Leu Pro Ala Gln Ser Thr Phe
1155                1160                1165
Thr Leu Ala Ile Ser Ala Tyr Ala Leu Ser Leu Gly Asp Lys
    1170                1175                1180
```